

WE CLAIM:

1. A method for identifying the probability of a molecular interaction within a biological network comprising:
  - (i) representing molecules as sets of conserved features;
  - (ii) computing the attraction probabilities between said features; and
  - (iv) using the computation of step (ii) to identify the probability of a molecular interaction within a biological network.
  
2. A method for identifying the probability of protein interactions within a biological network comprising:
  - (i) representing proteins as sets of conserved features;
  - (ii) computing the attraction probabilities between said features; and
  - (iv) using the computation of step (ii) to identify the probability of a molecular interaction within a biological network.
  
3. A method for identifying the probability of protein interactions within a biological network comprising:
  - (i) representing proteins as sets of conserved features;
  - (ii) computing the attraction probabilities between said features;
  - (iii) computing the attraction probabilities between proteins; and
  - (iv) using the computation of step (ii) and step (iii) to identify the probability of a molecular interaction within a biological network.

4. The method of claim 1, 2 or 3 further comprising computing the topology of a biological network wherein those networks displaying a more biologically realistic topology are assigned a greater probability.
5. The method of claim 1, 2 or 3 wherein the conserved features are protein domains or motifs.
6. The method of claim 1, 2 or 3 wherein the conserved features are nucleic acid molecule motifs.
7. The method of claim 2 or 3 wherein the attraction probabilities between features is computed using equation 6, 14, or 16.
8. The method of claim 2 wherein the attraction probabilities between proteins is accomplished using equation 5 or 17.
9. The method of claim 1 wherein the identification of a probability of a molecular interaction within a biological network is accomplished using equation 1.
10. The method of claim 2 or 3 wherein the identification of a probability of a protein interaction within a biological network is accomplished using equation 1.

11. The method of claim 4 wherein the topology of a biological network is determined using equation 2, 3, 4 or 7.
12. The method of claim 1 further comprising computing the posterior probabilities of interaction between a set of molecules.
13. The method of claim 2 further comprising computing the posterior probabilities of interaction between a set of proteins.
14. The method of claim 12 or 13 wherein a Markov Chain Monte Carlo technique is used to compute the posterior probabilities of interaction between a set of proteins.
15. The method of claim 12 or 13 wherein equation 1 is used to compute the posterior probabilities of interaction between a set of proteins.
16. A screening method for identification of a compound capable of modifying the interaction between at least two proteins comprising:
  - (i) identifying an interaction between at least two proteins using the method of claim 2 or 3 ;
  - (ii) contacting said proteins identified in step (i) with a test compound;
  - (iii) comparing the interaction of the proteins in the presence of the test compound with the interaction in the absence of the test compound;

wherein a difference in the interaction of the proteins in the presence of the test compound as compared to the interaction in the absence of a test compound indicates identification of a compound capable of modifying the interaction between proteins.

17. A screening method for identification of a compound capable of modifying the interaction between at least two molecules comprising:

- (i) identifying an interaction between at least molecules using the method of claim 1 ;
- (ii) contacting said molecules identified in step (i) with a test compound;
- (iii) comparing the interaction of the molecules in the presence of the

test compound with the interaction in the absence of the test compound; wherein a difference in the interaction of the molecules in the presence of the test compound as compared to the interaction in the absence of a test compound indicates identification of a compound capable of modifying the interaction between molecules.